



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Reed, John
- (ii) TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LONG, ALDRIDGE & NORMAN LLP
 - (B) STREET: Suite 600, 701 Pennsylvania Avenue, N.W.
 - (C) CITY: Washington
 - (D) STATE: District of Columbia
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/465,485
 - (B) FILING DATE: 05-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/124,256
 - (B) FILING DATE: 20-SEP-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/840,716
 - (B) FILING DATE: 21-FEB-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/288,692
 - (B) FILING DATE: 22-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Steven B. Kelber
 - (B) REGISTRATION NUMBER: 30,073
 - (C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 624-1200
 - (B) TELEFAX: (202) 624-1298

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTCCC

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTTCCTCT GGGAAGGATG GCGCACGCTG GGAGA

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATGCACCTA CCCAGCCTCC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACGGGGTACG GAGGCTGGGT AGGTGCATCT GGT

33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAAGGCAT CCTGCAGTTG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCCCAACTG CAGGATGCCT TTGTGGAAC GTACGG

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAAGGATG GCGCACGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGTGCGAC CCTCTTG

17

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACCGCGTGC GACCCTC

17

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCCTACCGCG TGCGACC

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTTCCTACC GCGTGCG

17

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCCTTCCT ACCGCGT

17

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACCCTT CCTACCG

17

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCGGCAG CGCGG

15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGCGGGGCG ACGGA

15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGAGCGCG GCGGGC

16

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCTCCCAGCG TGCGCCAT

18

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACTCACG CTCGGCCT

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCCCGCCC	CTCCGCGCCG	CCTGCCCCGCC	CGCCCGCCGC	GCTCCCGCCC	GCCGCTCTCC	60
GTGGCCCCGC	CGCGCTGCCG	CCGCCGCCGC	TGCCAGCGAA	GGTGCCGGGG	CTCCGGGCCC	120
TCCCTGCCGG	CGGCCGTCAG	CGCTCGGAGC	GAAGTGC GCG	ACGGGAGGTC	CGGGAGGCGA	180
CCGTAGTCGC	GCCGCCGCGC	AGGACCAGGA	GGAGGAGAAA	GGGTGCGCAG	CCCGGAGGCG	240
GGGTGCGCCG	GTGGGGTGCA	GCGGAAGAGG	GGGTCCAGGG	GGGAGAACTT	CGTAGCAGTC	300
ATCCTTTTTA	GGAAAAGAGG	GAAAAAATAA	AACCCTCCCC	CACCACCTCC	TTCTCCCCAC	360
CCCTCGCCGC	ACCACACACA	GCGCGGGCTT	CTAGCGCTCG	GCACCGGCGG	GCCAGGCGCG	420
TCCTGCCTTC	ATTTATCCAG	CAGCTTTTCG	GAAAATGCAT	TTGCTGTTTC	GAGTTTAATC	480
AGAAGACGAT	TCCTGCCTCC	GTCCCCGGCT	CCTTCATCGT	CCCATCTCCC	CTGTCTCTCT	540
CCTGGGGAGG	CGTGAAGCGG	TCCCGTGGAT	AGAGATTCAT	GCCTGTGTCC	GCGCGTGTGT	600
GCGCGCGTAT	AAATTGCCGA	GAAGGGGAAA	ACATCACAGG	ACTTCTGCGA	ATACCGGACT	660
GAAAATTGTA	ATTCATCTGC	CGCCGCCGCT	GCCAAAAAAA	AACTCGAGCT	CTTGAGATCT	720
CCGGTTGGGA	TTCTGCGGA	TTGACATTTC	TGTGAAGCAG	AAGTCTGGGA	ATCGATCTGG	780
AAATCCTCCT	AATTTTTACT	CCCTCTCCCC	CCGACTCCTG	ATTCATTGGG	AAGTTTCAAA	840
TCAGCTATAA	CTGGAGAGTG	CTGAAGATTG	ATGGGATCGT	TGCCTTATGC	ATTTGTTTTG	900
GTTTTACAAA	AAGGAAACTT	GACAGAGGAT	CATGCTGTAC	TTAAAAAATA	CAAGTAAGTC	960
TCGCACAGGA	AATTGGTTTA	ATGTAAC TTT	CAATGGAAAC	CTTTGAGATT	TTTTACTTAA	1020
AGTGCATTTC	AGTAAATTTA	ATTTCCAGGC	AGCTTAATAC	ATTGTTTTTA	GCCGTGTTAC	1080
TTGTAGTGTG	TATGCCCTGC	TTTCACTCAG	TGTGTACAGG	GAAACGCACC	TGATTTTTTA	1140
CTTATTAGTT	TGTTTTTTCT	TTAACCTTTC	AGCATCACAG	AGGAAGTAGA	CTGATATTAA	1200
CAATACTTAC	TAATAATAAC	GTGCCTCATG	AAATAAAGAT	CCGAAAGGAA	TTGGAATAAA	1260
AATTCCTGCT	GTCTCATGCC	AAGAGGGGAA	CACCAGAATC	AAGTGTTCCG	CGTGATTGAA	1320
GACACCCCCT	CGTCCAAGAA	TGCAAAGCAC	ATCCAATAAA	ATAGCTGGAT	TATAACTCCT	1380
CTTCTTTCTC	TGGGGGCCGT	GGGGTGGGAG	CTGGGGCGAG	AGGTGCCGTT	GGCCCCCGTT	1440
GCTTTTCCTC	TGGGAAGGAT	GGCGCACGCT	GGGAGAACGG	GGTACGACAA	CCGGGAGATA	1500
GTGATGAAGT	ACATCCATTA	TAAGCTGTCG	CAGAGGGGCT	ACGAGTGGGA	TGCGGGAGAT	1560
GTGGGCGCCG	CGCCCCCGGG	GGCCGCCCCC	GCACCGGGCA	TCTTCTCCTC	CCAGCCCCGGG	1620
CACACGCCCC	ATCCAGCCGC	ATCCCGCGAC	CCGGTCGCCA	GGACCTCGCC	GCTGCAGACC	1680

CCGGCTGCCC	CCGGCGCCGC	CGCGGGGCCT	GCGCTCAGCC	CGGTGCCACC	TGTGGTCCAC	1740
CTGGCCCTCC	GCCAAGCCGG	CGACGACTTC	TCCCGCCGCT	ACCGCGGCGA	CTTCGCCGAG	1800
ATGTCCAGCC	AGCTGCACCT	GACGCCCTTC	ACCGCGCGGG	GACGCTTTGC	CACGGTGGTG	1860
GAGGAGCTCT	TCAGGGACGG	GGTGAACCTGG	GGGAGGATTG	TGGCCTTCTT	TGAGTTCGGT	1920
GGGGTCATGT	GTGTGGAGAG	CGTCAACCGG	GAGATGTCGC	CCCTGGTGGA	CAACATCGCC	1980
CTGTGGATGA	CTGAGTACCT	GAACCGGCAC	CTGCACACCT	GGATCCAGGA	TAACGGAGGC	2040
TGGGATGCCT	TTGTGGAACT	GTACGGCCCC	AGCATGCGGC	CTCTGTTTGA	TTTCTCCTGG	2100
CTGTCTCTGA	AGACTCTGCT	CAGTTTGGCC	CTGGTGGGAG	CTTGCAACAC	CCTGGGTGCC	2160
TATCTGAGCC	ACAAGTGAAG	TCAACATGCC	TGCCCCAAAC	AAATATGCAA	AAGGTTCACT	2220
AAAGCAGTAG	AAATAATATG	CATTGTCAGT	GATGTACCAT	GAAACAAAGC	TGCAGGCTGT	2280
TTAAGAAAAA	ATAACACACA	TATAAACATC	ACACACACAG	ACAGACACAC	ACACACACAA	2340
CAATTAACAG	TCTTCAGGCA	AAACGTCGAA	TCAGCTATTT	ACTGCCAAAG	GGAAATATCA	2400
TTTATTTTTT	ACATTATTAA	GAAAAAAGAT	TTATTTATTT	AAGACAGTCC	CATCAAAACT	2460
CCGTCTTTGG	AAATCCGACC	ACTAATTGCC	AAACACCGCT	TCGTGTGGCT	CCACCTGGAT	2520
GTTCTGTGCC	TGTAAACATA	GATTCGCTTT	CCATGTTGTT	GGCCGGATCA	CCATCTGAAG	2580
AGCAGACGGA	TGGAAAAAGG	ACCTGATCAT	TGGGGAAGCT	GGCTTTCTGG	CTGCTGGAGG	2640
CTGGGGAGAA	GGTGTTCAAT	CACTTGCATT	TCTTTGCCCT	GGGGGCGTGA	TATTAACAGA	2700
GGGAGGGTTC	CCGTGGGGGG	AAGTCCATGC	CTCCCTGGCC	TGAAGAAGAG	ACTCTTTGCA	2760
TATGACTCAC	ATGATGCATA	CCTGGTGGGA	GGAAAAGAGT	TGGGAACTTC	AGATGGACCT	2820
AGTACCCACT	GAGATTTCCA	CGCCGAAGGA	CAGCGATGGG	AAAAATGCCC	TTAAATCATA	2880
GGAAAGTATT	TTTTTAAGCT	ACCAATTGTG	CCGAGAAAAG	CATTTTAGCA	ATTTATACAA	2940
TATCATCCAG	TACCTTAAAC	CCTGATTGTG	TATATTCATA	TATTTTGGAT	ACGCACCCCC	3000
CAACTCCCAA	TACTGGCTCT	GTCTGAGTAA	GAAACAGAAT	CCTCTGGAAC	TTGAGGAAGT	3060
GAACATTTTCG	GTGACTTCCG	ATCAGGAAGG	CTAGAGTTAC	CCAGAGCATC	AGGCCGCCAC	3120
AAGTGCCTGC	TTTTAGGAGA	CCGAAGTCCG	CAGAACCTAC	CTGTGTCCCA	GCTTGGAGGC	3180
CTGGTCCTGG	AACTGAGCCG	GGCCCTCACT	GGCCTCCTCC	AGGGATGATC	AACAGGGTAG	3240
TGTGGTCTCC	GAATGTCTGG	AAGCTGATGG	ATGGAGCTCA	GAATTCCACT	GTCAAGAAAG	3300
AGCAGTAGAG	GGGTGTGGCT	GGGCCTGTCA	CCCTGGGGCC	CTCCAGGTAG	GCCCGTTTTTC	3360
ACGTGGAGCA	TAGGAGCCAC	GACCCTTCTT	AAGACATGTA	TCACTGTAGA	GGGAAGGAAC	3420

AGAGGCCCTG	GGCCTTCCTA	TCAGAAGGAC	ATGGTGAAGG	CTGGGAACGT	GAGGAGAGGC	3480
AATGGCCACG	GCCCATTTTG	GCTGTAGCAC	ATGGCACGTT	GGCTGTGTGG	CCTTGGCCAC	3540
CTGTGAGTTT	AAAGCAAGGC	TTTAAATGAC	TTTGGAGAGG	GTCACAAATC	CTAAAAGAAG	3600
CATTGAAGTG	AGGTGTCATG	GATTAATTGA	CCCCTGTCTA	TGGAATTACA	TGTAAAACAT	3660
TATCTTGTC	CTGTAGTTTG	GTTTTATTTG	AAAACCTGAC	AAAAAAAAG	TTCCAGGTGT	3720
GGAATATGGG	GGTTATCTGT	ACATCCTGGG	GCATTAAAAA	AAAATCAATG	GTGGGGAACT	3780
ATAAAGAAGT	AACAAAAGAA	GTGACATCTT	CAGCAAATAA	ACTAGGAAAT	TTTTTTTTCT	3840
TCCAGTTTAG	AATCAGCCTT	GAAACATTGA	TGGAATAACT	CTGTGGCATT	ATTGCATTAT	3900
ATACCATTTA	TCTGTATTAA	CTTTGGAATG	TACTCTGTTC	AATGTTTAAT	GCTGTGGTTG	3960
ATATTTTCGAA	AGCTGCTTTA	AAAAAATACA	TGCATCTCAG	CGTTTTTTTG	TTTTTAATTG	4020
TATTTAGTTA	TGGCCTATAC	ACTATTTGTG	AGCAAAGGTG	ATCGTTTTCT	GTTTGAGATT	4080
TTTATCTCTT	GATTCTTCAA	AAGCATCTG	AGAAGGTGAG	ATAAGCCCTG	AGTCTCAGCT	4140
ACCTAAGAAA	AACCTGGATG	TCACTGGCCA	CTGAGGAGCT	TTGTTTCAAC	CAAGTCATGT	4200
GCATTTCCAC	GTCAACAGAA	TTGTTTATTG	TGACAGTTAT	ATCTGTTGTC	CCTTTGACCT	4260
TGTTTCTTGA	AGGTTTCCTC	GTCCCTGGGC	AATTCCGCAT	TTAATTCATG	GTATTCAGGA	4320
TTACATGCAT	GTTTGGTTAA	ACCCATGAGA	TTCATTCAGT	TAAAAATCCA	GATGGCGAAT	4380
GACCAGCAGA	TTCAAATCTA	TGGTGGTTTG	ACCTTTAGAG	AGTTGCTTTA	CGTGGCCTGT	4440
TTCAACACAG	ACCCACCCAG	AGCCCTCCTG	CCCTCCTTCC	GCGGGGGCTT	TCTCATGGCT	4500
GTCCTTCAGG	GTCTTCCTGA	AATGCAGTGG	TCGTTACGCT	CCACCAAGAA	AGCAGGAAAC	4560
CTGTGGTATG	AAGCCAGACC	TCCCCGGCGG	GCCTCAGGGA	ACAGAATGAT	CAGACCTTTG	4620
AATGATTCTA	ATTTTAAAGC	AAAATATTAT	TTTATGAAAG	GTTTACATTG	TCAAAGTGAT	4680
GAATATGGAA	TATCCAATCC	TGTGCTGCTA	TCCTGCCAAA	ATCATTTTAA	TGGAGTCAGT	4740
TTGCAGTATG	CTCCACGTGG	TAAGATCCTC	CAAGCTGCTT	TAGAAGTAAC	AATGAAGAAC	4800
GTGGACGTTT	TTAATATAAA	GCCTGTTTTG	TCTTTTGTTG	TTGTTCAAAC	GGGATTCACA	4860
GAGTATTTGA	AAAATGTATA	TATATTAAGA	GGTCACGGGG	GCTAATTGCT	AGCTGGCTGC	4920
CTTTTGCTGT	GGGGTTTTGT	TACCTGGTTT	TAATAACAGT	AAATGTGCCC	AGCCTCTTGG	4980
CCCCAGAACT	GTACAGTATT	GTGGCTGCAC	TTGCTCTAAG	AGTAGTTGAT	GTTGCATTTT	5040
CCTTATTGTT	AAAACATGT	TAGAAGCAAT	GAATGTATAT	AAAAGC		5086

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG	GCG	CAC	GCT	GGG	AGA	ACG	GGG	TAC	GAC	AAC	CGG	GAG	ATA	GTG	ATG	48
Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met	
1				5					10					15		
AAG	TAC	ATC	CAT	TAT	AAG	CTG	TCG	CAG	AGG	GGC	TAC	GAG	TGG	GAT	GCG	96
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala	
			20					25					30			
GGA	GAT	GTG	GGC	GCC	GCG	CCC	CCG	GGG	GCC	GCC	CCC	GCA	CCG	GGC	ATC	144
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile	
		35					40					45				
TTC	TCC	TCC	CAG	CCC	GGG	CAC	ACG	CCC	CAT	CCA	GCC	GCA	TCC	CGC	GAC	192
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp	
	50					55				60						
CCG	GTC	GCC	AGG	ACC	TCG	CCG	CTG	CAG	ACC	CCG	GCT	GCC	CCC	GGC	GCC	240
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala	
65					70					75					80	
GCC	GCG	GGG	CCT	GCG	CTC	AGC	CCG	GTG	CCA	CCT	GTG	GTC	CAC	CTG	GCC	288
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala	
				85					90					95		
CTC	CGC	CAA	GCC	GGC	GAC	GAC	TTC	TCC	CGC	CGC	TAC	CGC	GGC	GAC	TTC	336
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe	
		100						105					110			
GCC	GAG	ATG	TCC	AGC	CAG	CTG	CAC	CTG	ACG	CCC	TTC	ACC	GCG	CGG	GGA	384
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly	
		115					120					125				
CGC	TTT	GCC	ACG	GTG	GTG	GAG	GAG	CTC	TTC	AGG	GAC	GGG	GTG	AAC	TGG	432
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	
	130					135					140					
GGG	AGG	ATT	GTG	GCC	TTC	TTT	GAG	TTC	GGT	GGG	GTC	ATG	TGT	GTG	GAG	480
Gly	Arg	Ile	Val	Ala	Phe	Phe	Glu	Phe	Gly	Gly	Val	Met	Cys	Val	Glu	
145					150					155					160	

AGC	GTC	AAC	CGG	GAG	ATG	TCG	CCC	CTG	GTG	GAC	AAC	ATC	GCC	CTG	TGG	528
Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	Asn	Ile	Ala	Leu	Trp	
				165					170					175		
ATG	ACT	GAG	TAC	CTG	AAC	CGG	CAC	CTG	CAC	ACC	TGG	ATC	CAG	GAT	AAC	576
Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	Trp	Ile	Gln	Asp	Asn	
			180					185					190			
GGA	GGC	TGG	GAT	GCC	TTT	GTG	GAA	CTG	TAC	GGC	CCC	AGC	ATG	CGG	CCT	624
Gly	Gly	Trp	Asp	Ala	Phe	Val	Glu	Leu	Tyr	Gly	Pro	Ser	Met	Arg	Pro	
		195					200					205				
CTG	TTT	GAT	TTC	TCC	TGG	CTG	TCT	CTG	AAG	ACT	CTG	CTC	AGT	TTG	GCC	672
Leu	Phe	Asp	Phe	Ser	Trp	Leu	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Leu	Ala	
	210					215					220					
CTG	GTG	GGA	GCT	TGC	ATC	ACC	CTG	GGT	GCC	TAT	CTG	AGC	CAC	AAG		717
Leu	Val	Gly	Ala	Cys	Ile	Thr	Leu	Gly	Ala	Tyr	Leu	Ser	His	Lys		
225					230					235						

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met
1				5					10					15	
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala
			20					25					30		
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile
		35					40					45			
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp
	50					55					60				
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala
	65				70					75					80
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala
				85					90					95	
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe
			100					105					110		
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly
		115					120					125			
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp
	130					135					140				

Gly 145	Arg	Ile	Val	Ala	Phe 150	Phe	Glu	Phe	Gly	Gly 155	Val	Met	Cys	Val	Glu 160
Ser	Val	Asn	Arg	Glu 165	Met	Ser	Pro	Leu	Val 170	Asp	Asn	Ile	Ala	Leu 175	Trp
Met	Thr	Glu	Tyr 180	Leu	Asn	Arg	His	Leu 185	His	Thr	Trp	Ile	Gln 190	Asp	Asn
Gly	Gly	Trp	Asp	Ala	Phe	Val	Glu 200	Leu	Tyr	Gly	Pro	Ser 205	Met	Arg	Pro
Leu	Phe	Asp	Phe	Ser	Trp	Leu 215	Ser	Leu	Lys	Thr	Leu 220	Leu	Ser	Leu	Ala
Leu 225	Val	Gly	Ala	Cys	Ile 230	Thr	Leu	Gly	Ala	Tyr 235	Leu	Ser	His	Lys	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG	GCG	CAC	GCT	GGG	AGA	ACG	GGG	TAC	GAC	AAC	CGG	GAG	ATA	GTG	ATG	48
Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met	
1				5					10					15		
AAG	TAC	ATC	CAT	TAT	AAG	CTG	TCG	CAG	AGG	GGC	TAC	GAG	TGG	GAT	GCG	96
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala	
			20					25					30			
GGA	GAT	GTG	GGC	GCC	GCG	CCC	CCG	GGG	GCC	GCC	CCC	GCA	CCG	GGC	ATC	144
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile	
			35				40					45				
TTC	TCC	TCC	CAG	CCC	GGG	CAC	ACG	CCC	CAT	CCA	GCC	GCA	TCC	CGC	GAC	192
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp	
			50			55					60					
CCG	GTC	GCC	AGG	ACC	TCG	CCG	CTG	CAG	ACC	CCG	GCT	GCC	CCC	GGC	GCC	240
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala	
65					70					75				80		

GCC	GCG	GGG	CCT	GCG	CTC	AGC	CCG	GTG	CCA	CCT	GTG	GTC	CAC	CTG	GCC	288
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala	
				85					90					95		
CTC	CGC	CAA	GCC	GGC	GAC	GAC	TTC	TCC	CGC	CGC	TAC	CGC	GGC	GAC	TTC	336
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe	
			100					105					110			
GCC	GAG	ATG	TCC	AGC	CAG	CTG	CAC	CTG	ACG	CCC	TTC	ACC	GCG	CGG	GGA	384
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly	
		115					120					125				
CGC	TTT	GCC	ACG	GTG	GTG	GAG	GAG	CTC	TTC	AGG	GAC	GGG	GTG	AAC	TGG	432
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	
	130					135					140					
GGG	AGG	ATT	GTG	GCC	TTC	TTT	GAG	TTC	GGT	GGG	GTC	ATG	TGT	GTG	GAG	480
Gly	Arg	Ile	Val	Ala	Phe	Phe	Glu	Phe	Gly	Gly	Val	Met	Cys	Val	Glu	
145					150					155					160	
AGC	GTC	AAC	CGG	GAG	ATG	TCG	CCC	CTG	GTG	GAC	AAC	ATC	GCC	CTG	TGG	528
Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	Asn	Ile	Ala	Leu	Trp	
				165					170					175		
ATG	ACT	GAG	TAC	CTG	AAC	CGG	CAC	CTG	CAC	ACC	TGG	ATC	CAG	GAT	AAC	576
Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	Trp	Ile	Gln	Asp	Asn	
			180					185					190			
GGA	GGC	TGG	GTA	GGT	GCA	TCT	GGT	GAT	GTG	AGT	CTG	GGC				615
Gly	Gly	Trp	Val	Gly	Ala	Ser	Gly	Asp	Val	Ser	Leu	Gly				
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met	
1				5					10					15		
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala	
			20					25					30			
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile	
		35					40					45				
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp	
	50					55					60					
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala	
65					70					75					80	

Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala	85	90	95
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe	100	105	110
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly	115	120	125
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	130	135	140
Gly	Arg	Ile	Val	Ala	Phe	Phe	Glu	Phe	Gly	Gly	Val	Met	Cys	Val	Glu	145	150	155
Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	Asn	Ile	Ala	Leu	Trp	165	170	175
Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	Trp	Ile	Gln	Asp	Asn	180	185	190
Gly	Gly	Trp	Val	Gly	Ala	Ser	Gly	Asp	Val	Ser	Leu	Gly				195	200	205

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: Synthetic DNA
- (iv) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: Modified_base
 - (B) LOCATION: 16..17
 - (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCTCCCAGCG TGCGCCAT

18

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: Synthetic DNA
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Modified_base
 - (B) LOCATION: 16..17
 - (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGCACTCACG CTCGGCCT

18

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: Synthetic DNA
- (iv) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: Modified_base
 - (B) LOCATION: 18..19
 - (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCGGCGGG CGGGCGGGCA

20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other nucleic acid;
 - (A) DESCRIPTION: Synthetic DNA
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Modified_base
 - (B) LOCATION: 18..19
 - (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGCGGAGGC CGGCCGGCGG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: Modified_base
- (B) LOCATION: 18..19
- (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCGGCGGCG GCGGCAGCGC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: Modified_base
- (B) LOCATION: 18..19
- (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCCGGGAA GGGCGCCCGC

20